SVEPM 2018— Classic problems, future focus, and engagement of stakeholders in veterinary epidemiology and economics, Society of Veterinary Epidemiology and Preventive Medicine conference Tallinn, Estonia 21st–23rd March 2018

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The 2018 Annual Meeting of the Society for Veterinary Epidemiology and Preventive Medicine (SVEPM), held in Tallinn, Estonia, highlighted emerging techniques in veterinary epidemiology and economics, whilst also facilitating discussion of classic problems and methods to engage stakeholders. Workshops included: the use of Directed Acyclic Graphs; interactive data visualisation; digital data and surveillance; Big Data epidemiology; an introduction to Conjoint Analysis; and a discussion on the future of veterinary epidemiology. From within the conference programme, the seven papers contained in this Special Issue of Preventive Veterinary Medicine demonstrate the excellent platform for networking between veterinary epidemiologists, public health professionals, economists and aligned professionals which this conference provides.

Topics included: a systematic literature review to characterise One Health surveillance systems; an investigation into the causes and characteristics of African Swine Fever (ASF) outbreaks in domestic pigs in Estonia; combining genome information and contact-tracing to improve detection of *Salmonella* Dublin transmission in cattle; the use of network analysis to examine social networks of free-roaming domestic dogs; estimating the probability of disease freedom at the herd-level for bovine respiratory syncytial virus and bovine coronavirus; characterising herd typologies for Danish sow herds based on biosecurity, productivity, antimicrobial and vaccine use; and the impact of dam status on *Mycobacterium avium* subspecies *paratuberculosis* infection in calves.

In their work, Bordier et al. (2018) worked to improve understanding of the practical application, outcomes and impacts of using a One Health (OH) ethos in disease surveillance systems. By reviewing information on existing OH surveillance systems, they defined their organisational and functional characteristics, the context for- and likely factors involved in implementation and performance of surveillance systems. This enabled identification of different dimensions of surveillance, areas of collaboration, barriers and levers to progress. The authors then established a conceptual framework for use when describing and evaluating on-going - or when developing future - OH surveillance systems.

In examining recently emerged ASF in domestic pigs in Estonia, Nurmoja et al. (2018) established the epidemiology of the outbreaks and links to disease in wild boar. They estimated the high-risk period for farms using interviews, then investigated the clinical manifestation, possible origins and modes

of virus introduction. Herd incidence and outbreak risk were calculated in domestic pigs, with spatial and temporal distribution then characterised for this population. Thereafter, the domestic's distribution was used in Bayesian modelling of ASF occurrence in wild boar. Mild, non-specific (to ASF) clinical symptoms masked a high virus virulence, with backyard producers suffering greatest morbidity and mortality. Study findings suggest indirect modes of transmission which are difficult to identify and probably are linked to biosecurity issues. Finally, the spatio-temporal modelling suggested a link between ASF in domestic pigs and local wild boar, which has important implications for future disease control.

A new method to detect between-herd livestock movements, particularly useful if movements between herds within business units are not recorded, was reported by de Knegt et al. (2018). They grouped animal movements into livestock business-units based on ownership and location, then tested their technique using incomplete movement records and genome sequencing of *Salmonella* Dublin isolates. They found higher probabilities of infectious animal introduction in businesses with the same clone of *S.* Dublin, compared to those with non-related strains. This substantiates the use of business-units rather than individual herds for disease tracing tasks in livestock movements.

Network analysis was also used to identify social structures in Torres Strait island free-ranging dog populations. The dogs' social networks had 'small-world' structures; clustering and low average path lengths between individuals. Three networks were highly connected, but their characteristics (centrality and duration of association) differed by community. These differences have implications for the transmission parameters associated with disease spread in dog populations, providing a foundation for future modelling; for more information see Brookes et al. (2018).

Changes in the probability of freedom from antibodies found in bulk tank milk (BTM) with time since testing, were estimated by Toftaker et al. (2018), in order to consolidate disease-free status ascertained in a national control program against bovine respiratory syncytial virus (BRSV) and bovine coronavirus (BCV) in Norway. Included in the probability of freedom analyses were test sensitivity, real animal movement and regional herd prevalence data, used to estimate the probability of infection introduction from purchased animals, and local transmission. The outputs were used to validate herd-level estimates of subsequent BTM testing. The probability of freedom declined with post-testing, and was impacted by animal purchasing, for BTM test-negative herds. Comparison of probability of freedom estimates and previous BTM test-results suggest that the former is a better appraisal of herd-level BTM status for both pathogens. This information can be used to improve the efficiency of future control measures against BRSV and BCV.

A decision by the EU Commission to phase out use of zinc oxide by 2022 has complicated efforts to reduce antimicrobial use (AMU) in pigs. To best inform future AMU whilst sustaining production, Kruse et al. (2018) established herd typologies based on biosecurity, productivity, vaccination and AMU information collated from telephone interviews and secondary use of husbandry data. They then discussed feasible strategies for each typology which aimed to improve pig health whilst reducing AMU without hampering animal welfare. Discussion of these characteristics will be useful to inform future husbandry practices in Denmark, with implications for other national pig herds.

The lack of understanding about the relative importance of transmission routes for *Mycobacterium avium* subspecies *paratuberculosis* (MAP), which causes Johne's disease, hinders control schemes for this endemic infection in the UK. Using a cohort study design to ameliorate the long incubation period of Johne's disease, milking cows were routinely monitored for MAP using milk ELISA testing. The relative importance of dam MAP status compared to other risk factors was then examined, after the relationship with time until first detection of infection had been characterised. The study results

suggest that cows may be transmitting MAP to their offspring earlier in the cows' infection course than previously understood. This has practical implications for on-farm management of MAP-positive animals' offspring; for more information see Patterson et al. (2019).

This special issue of Preventive Veterinary Medicine represents progress in research which fosters knowledge sharing to improve the health of animals, humans and the environment. Thank you to the members of the local organising committee in Tallinn for hosting a marvellous conference in a stunning location. We greatly acknowledge all reviewers for their help in evaluating manuscripts submitted to this special issue of Preventive Veterinary Medicine.

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